I hereby certify that this correspondence is being electronically filed in the United States Patent and Trademark Office on January 24, 2011.

Frank C. Eisenschenk, Ph.D., Patent Attorney

REQUEST FOR CERTIFICATE OF CORRECTION UNDER 37 CFR 1.322
Docket No. ISI.103

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Simon Davis
Issued	:	December 14, 2010
Patent No.	:	7,851,598
Conf. No.	:	4177
For	:	Receptor Modulators

Mail Stop Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

REQUEST FOR CERTIFICATE OF CORRECTION
UNDER 37 CFR 1.322 (OFFICE MISTAKE)

Sir:

A Certificate of Correction for the above-identified patent has been prepared and is attached hereto.

In the left-hand column below is the column and line number where errors occurred in the patent. In the right-hand column is the page and line number in the application where the correct information appears.

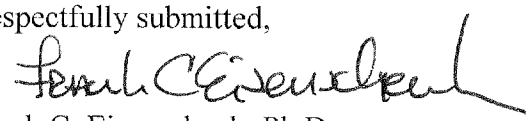
Patent Reads:	**Application Reads:**
Column 8, line 33:	Page 12, line 15:
"(Yxx/Ix_{7-12}YxxL/I)"	--(YxxL/Ix_{7-12}YxxL/I)--
Column 13, line 13:	Page 20, line 2:
"(http://www.ncbi.nhn.nih.gov/)"	--(http://www.ncbi.nlm.nih.gov/)--

Column 18, line 11:	Page 27, line 25:
"cysteine ● HC1"	--cysteine•HC1--
Column 18, line 14:	Page 27, line 28:
"cysteine-HC1"	--cysteine•HC1--
Column 22, Table 1, Column "Protein":	Page 34, Table 1, Column "Protein":
"hpd-1"	--hPD-1--
Column 45, Table 4, Row "ATOM 890":	Page 52, Table 4, Row "ATOM 890":
"41.625"	--41.525--
Column 49, Table 4, Row "ATOM 1016":	Page 55, Table 4, Row "ATOM 1016":
"46.58"	--46.88--
Column 133, Table 5, line 11:	Page 116, Table 5, line 11:
"tattatttc tgggtcgagga"	--tattattttc tgggtgagga--.

A true and correct copy of pages 12, 20, 27, 34, 52, 55, and 116 of the specification as filed which support Applicant's assertion of the errors on the part of the Patent Office accompanies this Certificate of Correction.

Approval of the Certificate of Correction is respectfully requested.

Respectfully submitted,



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FCE/jb
Attachments: Copy of pages 12, 20, 27, 34, 52, 55, and 116 of the specification
Certificate of Correction

only the C'-D loop of CD28. The second type of chimeric protein may be one which does not bind to any portion of the C'-D loop of CD28. The second type of chimeric protein may or may not bind to the C'-D loop (or the equivalent loop) of any other member of the CD28 family of proteins. The second type of protein may or may not bind to any or all of the sequences shown in Table 3.

Receptors bound by the antibody and chimeric protein

The receptors which are bound by the antibody or chimeric protein of the invention are expressed on the cell surface. The receptor is capable of being phosphorylated (typically at one or more tyrosine residues in the cytoplasmic region of the receptor), and phosphorylation of the receptor will typically lead to its activation. The receptor will comprise a cytoplasmic domain that is dependent on extrinsic protein kinases to be phosphorylated. Thus the receptor will not have an intrinsic enzymatic (kinase or phophatase) activity. The receptor will typically comprise tyrosine-containing, activating ITAM motifs ($YxxL/Ix_{7-12}YxxL/I$), inhibitory ITIM motifs (I/V/L/SxYxxL/V) or "switch" (TxYxxV/I; activating and inhibitory) signalling motifs (where x is any amino acid). These motifs are phosphorylated by cytoplasmic tyrosine kinases, such as the Src kinases, in competition with antagonistic tyrosine phosphatases, such as CD45. The signalling character of the receptors is defined exclusively by the nature of these motifs (ITAM vs ITIM: activating vs inhibitory).

The receptor may be a member of any surface protein superfamily, but is typically a member of the immunoglobulin superfamily. The receptor may be a member of the CD28 superfamily. The receptor may be any of the specific receptors which are shown in Table 1 or 2 or may comprise a sequence which is homologous to the sequence of any of these specific receptors. The receptor may be CD28, CTLA-4, ICOS, PD-1 or BTLA or comprise a sequence which is homologous to the sequence of any of these specific receptors.

The receptor may be of any of the species that are mentioned herein, and thus may be a mammalian or avian, preferably rodent (such as mouse or rat) or primate (such as human) receptor.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pair (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighbourhood word score threshold (Altschul *et al*, supra). These initial neighbourhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extensions for the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) *Proc. Natl. Acad. Sci.* USA 89: 10915-10919) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

The BLAST algorithm performs a statistical analysis of the similarity between two sequences; see e.g., Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90: 5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two amino acid sequences would occur by chance. For example, a sequence is considered similar to another sequence if the smallest sum probability in comparison of the first sequence to the second sequence is less than about 1, preferably less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

The homologous sequence typically differs by at least 1, 2, 5, 10, 20 or more mutations (each of which may be a substitution, deletion or insertion of an amino acid). These mutations may be measured across any of the regions mentioned above in relation to calculating homology. The substitutions are preferably conservative substitutions. These are defined according to the following Table. Amino acids in

(v) Purification of the CD28 homodimer

The pH of the thrombin-cleaved protein was adjusted to pH 8.5 using 2.75M Tris pH 8.5, prior to concentration to 0.5 ml using a Centriprep 10 concentrator (Millipore Corp). Fresh Protein A beads were washed and rehydrated to a final volume of ~5 mls, prior to being packed into a 0.7 cm x 20 cm Econo-column (Bio-Rad, U.K.) and then equilibriated with HBS, pH 8.5 at 4°C. The concentrated protein was then applied to the column, allowed to run into the bed, and then sequential fractions were eluted by addition of 0.5 ml of HBS, pH 8.5 to the top of the bed every 10 minutes for 2h. The absorbance of each fraction was determined at 280 nm. The extent of separation of the Fc from the thrombin-released CD28 homodimer was determined by 12% SDS-PAGE analysis of the fractions under non-reducing conditions. The critical steps for good separation were (1) to allow the protein to pass slowly through the column and (2) to conduct the separation at 4°C. The homodimer was concentrated to 0.5 ml and subjected to gel-filtration on a Superdex 75 H/R column (Amersham Biosciences). The purified homodimer was used for crystallization trials, reduced and alkylated for other crystallization trials (see below), or frozen at –80°C for future use.

Preparation of Fab fragments of 5.11A1 antibody

Fab fragments were prepared using the Pierce Biotechnology ImmunoPure® Fab Preparation Kit, as briefly outlined below.

(i) Fab fragment generation and purification

Nine millilitres of whole, purified 5.11A1 antibody at 0.3 mg/ml in PBS was concentrated to 1 ml and then diluted to 10 mls with 20 mM sodium phosphate, 10 mM EDTA, pH 7 and then re-concentrated to 0.5 ml. To this was added 0.5 ml of 20 mM sodium phosphate, pH 7 containing 3.5 mg/ml cysteine•HCl. The 1 ml mixture was then added to 0.5 ml of a 50% slurry of Sepharose-immobilized Papain supplied with the kit, which had been pre-equilibrated with 20 mM sodium phosphate pH 7 containing 3.5 mg/ml cysteine•HCl. This was then incubated for 5 hours in a shaking water bath at 37°C. The cleaved Fab and Fc fragments and undigested IgG were separated from the Immobilized Papain beads by centrifugation at 1000*g* and the beads rinsed with 1.5 ml of the ImmunoPure IgG Binding Buffer supplied with the kit. The wash was then combined with the crude digest and the mix applied to a Sepharose-immobilized Protein

Table 1

CD28 family superagonistic epitopes

Epitopes are named according to the strands from which they derive.

Protein	*A'*	*B*	*C-C'*	*C"-D*	*E*	*F*	*G*
hCD28	SPMLV	AVNLS	SLHKGLDSAVEVCV	VYSKTGFNCDG	FYLQN	TDIYFC	NGTIIHV
hCTLA-4	PAVVL	GIASFV	TVLRQADSQVTEVCA	FLDDSICTG	LTIQG	TGLYIC	NGTQIYV
hICOS	YEMFI	GVQIL	QLLKGGQILCD	VSIKSLKFCHS	FFLYN	ANYYFC	TGGYLHI

PD-1 and BTLA superagonistic epitopès

Protein	*A*	*B*	*C-C'*	*C"-D*	*E*	*F*	*G*
hPD-1	PALLVV	DNATF	RMSPSNQTDK	QPGQDCRFR	MSVVR	NDSGTY	LRAELR
hBTLA	QSEHSI	DPFEL	KLNG	QTSWK	LHFEP	NDNGSY	TTLYVT

Table 3

Protein	*Sequence*
hCD28	GNYSQQLQVYSKTGF
hCTLA-4	YMMGNELTFLDDS
hICOS	KTKGSGNTVSIKSLK
hPD-1	LAAFPEDRSQPGQDCR

ATOM	842	CB	ASP	110	158.395	60.740	62.082	1.00	68.55	L
ATOM	843	CG	ASP	110	157.861	61.528	60.889	1.00	84.17	L
ATOM	844	OD1	ASP	110	156.656	61.399	60.580	1.00	78.11	L
ATOM	845	OD2	ASP	110	158.641	62.277	60.256	1.00	94.16	L
ATOM	846	C	ASP	110	158.022	58.731	63.551	1.00	60.38	L
ATOM	847	O	ASP	110	158.093	58.882	64.776	1.00	54.97	L
ATOM	848	N	ALA	111	158.487	57.651	62.932	1.00	55.72	L
ATOM	849	CA	ALA	111	159.151	56.577	63.661	1.00	59.37	L
ATOM	850	CB	ALA	111	158.123	55.633	64.272	1.00	55.98	L
ATOM	851	C	ALA	111	160.074	55.815	62.730	1.00	51.95	L
ATOM	852	O	ALA	111	159.669	55.363	61.658	1.00	59.98	L
ATOM	853	N	ALA	112	161.328	55.685	63.141	1.00	47.00	L
ATOM	854	CA	ALA	112	162.318	54.977	62.348	1.00	42.20	L
ATOM	855	CB	ALA	112	163.712	55.266	62.887	1.00	43.77	L
ATOM	856	C	ALA	112	162.043	53.476	62.376	1.00	42.23	L
ATOM	857	O	ALA	112	161.447	52.957	63.325	1.00	45.43	L
ATOM	858	N	PRO	113	162.464	52.761	61.325	1.00	51.11	L
ATOM	859	CD	PRO	113	163.153	53.256	60.117	1.00	52.49	L
ATOM	860	CA	PRO	113	162.250	51.316	61.269	1.00	49.74	L
ATOM	861	CB	PRO	113	162.267	51.018	59.776	1.00	32.76	L
ATOM	862	CG	PRO	113	163.223	52.029	59.220	1.00	41.64	L
ATOM	863	C	PRO	113	163.356	50.568	61.997	1.00	45.33	L
ATOM	864	O	PRO	113	164.511	50.988	61.974	1.00	53.16	L
ATOM	865	N	THR	114	163.006	49.475	62.661	1.00	36.71	L
ATOM	866	CA	THR	114	164.009	48.675	63.341	1.00	39.49	L
ATOM	867	CB	THR	114	163.505	48.159	64.706	1.00	34.54	L
ATOM	868	OG1	THR	114	162.504	47.153	64.511	1.00	38.54	L
ATOM	869	CG2	THR	114	162.926	49.305	65.518	1.00	31.63	L
ATOM	870	C	THR	114	164.322	47.515	62.406	1.00	42.88	L
ATOM	871	O	THR	114	163.527	46.585	62.247	1.00	35.53	L
ATOM	872	N	VAL	115	165.488	47.596	61.769	1.00	36.33	L
ATOM	873	CA	VAL	115	165.939	46.594	60.815	1.00	42.49	L
ATOM	874	CB	VAL	115	166.973	47.210	59.839	1.00	46.96	L
ATOM	875	CG1	VAL	115	167.217	46.269	58.670	1.00	26.72	L
ATOM	876	CG2	VAL	115	166.470	48.555	59.338	1.00	30.46	L
ATOM	877	C	VAL	115	166.544	45.324	61.424	1.00	38.71	L
ATOM	878	O	VAL	115	167.064	45.327	62.541	1.00	36.49	L
ATOM	879	N	SER	116	166.458	44.237	60.659	1.00	44.76	L
ATOM	880	CA	SER	116	166.988	42.939	61.053	1.00	51.12	L
ATOM	881	CB	SER	116	165.975	42.188	61.913	1.00	55.78	L
ATOM	882	OG	SER	116	165.653	42.932	63.068	1.00	58.23	L
ATOM	883	C	SER	116	167.292	42.130	59.799	1.00	44.61	L
ATOM	884	O	SER	116	166.413	41.891	58.976	1.00	53.07	L
ATOM	885	N	ILE	117	168.547	41.726	59.641	1.00	40.79	L
ATOM	886	CA	ILE	117	168.935	40.929	58.487	1.00	35.02	L
ATOM	887	CB	ILE	117	170.299	41.393	57.902	1.00	20.96	L
ATOM	888	CG2	ILE	117	171.426	41.040	58.848	1.00	28.48	L
ATOM	889	CG1	ILE	117	170.529	40.742	56.537	1.00	16.89	L
ATOM	890	CD1	ILE	117	171.461	41.525	55.632	1.00	18.50	L
ATOM	891	C	ILE	117	169.039	39.484	58.952	1.00	32.15	L
ATOM	892	O	ILE	117	169.467	39.212	60.076	1.00	40.81	L
ATOM	893	N	PHE	118	168.626	38.560	58.091	1.00	28.82	L
ATOM	894	CA	PHE	118	168.671	37.145	58.423	1.00	22.76	L

ATOM	1001	O	VAL	133	166.701	39.222	56.454	1.00	24.39	L
ATOM	1002	N	CYS	134	165.206	40.404	55.254	1.00	24.79	L
ATOM	1003	CA	CYS	134	165.412	41.626	55.999	1.00	33.03	L
ATOM	1004	C	CYS	134	164.070	42.163	56.444	1.00	34.77	L
ATOM	1005	O	CYS	134	163.166	42.338	55.631	1.00	37.02	L
ATOM	1006	CB	CYS	134	166.104	42.660	55.127	1.00	37.32	L
ATOM	1007	SG	CYS	134	166.705	44.083	56.077	1.00	64.48	L
ATOM	1008	N	PHE	135	163.946	42.420	57.737	1.00	28.41	L
ATOM	1009	CA	PHE	135	162.710	42.949	58.296	1.00	35.98	L
ATOM	1010	CB	PHE	135	162.297	42.152	59.536	1.00	23.45	L
ATOM	1011	CG	PHE	135	161.854	40.746	59.244	1.00	41.99	L
ATOM	1012	CD1	PHE	135	160.991	40.472	58.187	1.00	58.79	L
ATOM	1013	CD2	PHE	135	162.280	39.696	60.049	1.00	38.90	L
ATOM	1014	CE1	PHE	135	160.555	39.170	57.939	1.00	56.32	L
ATOM	1015	CE2	PHE	135	161.849	38.391	59.810	1.00	57.18	L
ATOM	1016	CZ	PHE	135	160.987	38.127	58.753	1.00	46.88	L
ATOM	1017	C	PHE	135	162.880	44.412	58.696	1.00	37.21	L
ATOM	1018	O	PHE	135	163.841	44.773	59.373	1.00	31.75	L
ATOM	1019	N	LEU	136	161.951	45.253	58.264	1.00	38.27	L
ATOM	1020	CA	LEU	136	161.968	46.665	58.622	1.00	33.10	L
ATOM	1021	CB	LEU	136	162.049	47.531	57.369	1.00	23.62	L
ATOM	1022	CG	LEU	136	163.303	47.259	56.534	1.00	17.58	L
ATOM	1023	CD1	LEU	136	163.055	46.103	55.572	1.00	17.79	L
ATOM	1024	CD2	LEU	136	163.686	48.512	55.770	1.00	29.81	L
ATOM	1025	C	LEU	136	160.632	46.839	59.319	1.00	30.65	L
ATOM	1026	O	LEU	136	159.600	47.002	58.673	1.00	30.43	L
ATOM	1027	N	ASN	137	160.651	46.779	60.643	1.00	35.92	L
ATOM	1028	CA	ASN	137	159.421	46.873	61.400	1.00	43.25	L
ATOM	1029	CB	ASN	137	159.387	45.751	62.433	1.00	42.56	L
ATOM	1030	CG	ASN	137	159.308	44.384	61.793	1.00	30.61	L
ATOM	1031	OD1	ASN	137	159.471	43.356	62.454	1.00	37.72	L
ATOM	1032	ND2	ASN	137	159.057	44.363	60.490	1.00	39.03	L
ATOM	1033	C	ASN	137	159.101	48.199	62.075	1.00	40.01	L
ATOM	1034	O	ASN	137	159.975	49.028	62.305	1.00	39.51	L
ATOM	1035	N	ASN	138	157.813	48.362	62.370	1.00	41.07	L
ATOM	1036	CA	ASN	138	157.239	49.526	63.036	1.00	38.43	L
ATOM	1037	CB	ASN	138	157.227	49.273	64.540	1.00	34.91	L
ATOM	1038	CG	ASN	138	156.667	47.916	64.883	1.00	33.75	L
ATOM	1039	OD1	ASN	138	155.592	47.806	65.459	1.00	29.26	L
ATOM	1040	ND2	ASN	138	157.402	46.864	64.537	1.00	33.12	L
ATOM	1041	C	ASN	138	157.838	50.898	62.749	1.00	31.73	L
ATOM	1042	O	ASN	138	158.582	51.447	63.559	1.00	39.37	L
ATOM	1043	N	PHE	139	157.492	51.458	61.599	1.00	32.60	L
ATOM	1044	CA	PHE	139	157.982	52.770	61.227	1.00	34.36	L
ATOM	1045	CB	PHE	139	159.138	52.644	60.237	1.00	37.95	L
ATOM	1046	CG	PHE	139	158.770	51.972	58.946	1.00	21.99	L
ATOM	1047	CD1	PHE	139	158.295	52.716	57.869	1.00	28.23	L
ATOM	1048	CD2	PHE	139	158.941	50.597	58.792	1.00	23.34	L
ATOM	1049	CE1	PHE	139	157.998	52.102	56.651	1.00	22.39	L
ATOM	1050	CE2	PHE	139	158.646	49.969	57.578	1.00	15.56	L
ATOM	1051	CZ	PHE	139	158.175	50.723	56.505	1.00	21.70	L
ATOM	1052	C	PHE	139	156.868	53.626	60.627	1.00	42.27	L
ATOM	1053	O	PHE	139	155.772	53.142	60.350	1.00	50.50	L

Table 5

DNA sequence of human CD28 cDNA

```
agactctcag gccttggcag gtgcgtcttt cagttccgct cacacttcgg gttcctcggg      60
gaggaggggc tggaacccta gcccatcgtc aggacaaaga tgctcaggct gctcttggct     120
ctcaacttat tccgttcaat tcaagtaaca ggaaacaaga ttttggtgaa gcagtcgccc     180
atgcttgtag cgtacgacaa tgcggtcaac cttagctgca agtattccta caatctcttc     240
tcaagggagt tccgggcatc ccttcacaaa ggactggata gtgctgtgga agtctgtgtt     300
gtatatggga attactccca gcagcttcag gtttactcaa aaacggggtt caactgtgat     360
gggaaattgg gcaatgaatc agtgacattc tacctccaga atttgtatgt taaccaaaca     420
gatatttact tctgcaaaat tgaagttatg tatcctcctc cttacctaga caatgagaag     480
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc     540
ggaccttcta agcccttttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc     600
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg     660
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag     720
ccctatgccc caccacgcga cttcgcagcc tatcgctcct gacacggacg cctatccaga     780
agccagccgg ctggcagccc ccatctgctc aatatcactg ctctggatag gaaatgaccg     840
ccatctccag ccggccacct cagccgctgt tgggccacca atgccaattt ttctcgagtg     900
actagaccaa atatcaagat cattttgaga ctctgaaatg aagtaaaaga gatttcctgt     960
gacaggccaa gtcttacagt gccatggccc acattccaac ttaccatgta cttagtgact    1020
tgactgagaa gttagggtag aaaacaaaaa gggagtggat tctgggagcc tcttccgttt    1080
ctcactcacc tgcacatctc agtcaagcaa agtgtggtat ccacagacat tttagttgca    1140
gaagaaaggc taggaaatca ttccttttgg ttaaatgggt gtttaatctt ttggttagtg    1200
ggttaaacgg ggtaagttag agtaggggga gggataggaa gacatattta aaaaccatta    1260
aaacactgtc tcccactcat gaaatgagcc acgtagttcc tatttaatgc tgttttcctt    1320
tagtttagaa atacatagac attgtctttt atgaattctg atcatattta gtcattttga    1380
ccaaatgagg gatttggtca aatgagggat tccctcaaag caatatcagg taaaccaagt    1440
tgctttcctc actccctgtc atgagacttc agtgttaatg ttcacaatat actttcgaaa    1500
gaataaaata gttc                                                      1514
```

Amino acid sequence of human CD28 (SEQ ID NO:1)

MLRLLLALNL FPSIQVTGNK ILVKQSPMLV AYDNAVNLSC KYSYNLFSRE FRASLHKGLD
SAVEVCVVYG NYSQQLQVYS KTGFNCDGKL GNESVTFYLQ NLYVNQTDIY FCKIEVMYPP
PYLDNEKSNG TIIHVKGKHL CPSPLFPGPS KPFWVLVVVG GVLACYSLLV TVAFIIFWVR
SKRSRLLHSD YMNMTPRRPG PTRKHYQPYA PPRDFAAYRS

The extracellular domain is shown in bold
The stalk region is underlined

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 7,851,598

APPLICATION NO.: 10/585,491

DATED : December 14, 2010

INVENTOR : Simon Davis

It is certified that errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 8,
Line 33, "(Yxx/Ix_{7-12}YxxL/I)" should read --(YxxL/Ix_{7-12}YxxL/I)--.

Column 13,
Line 13, "(http://www.ncbi.nhn.nih.gov/)" should read
--(http://www.ncbi.nlm.nih.gov/)--.

Column 18,

Line 11, "cysteine ● HC1" should read -- cysteine•HC1--.
Line 14, "cysteine-HC1" should read --cysteine•HC1--.

Column 22,
Table 1, Column "Protein", "hpd-1" should read --hPD-1--.

Column 45,
Table 4, Row "ATOM 890", "41.625" should read --41.525--.

Column 49,
Table 4, Row "ATOM 1016", "46.58" should read --46.88--.

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UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO. : 7,851,598

APPLICATION NO.: 10/585,491

DATED : December 14, 2010

INVENTOR : Simon Davis

It is certified that errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 133,
Table 5, Line 11, "tattatttc tgggtcgagga" should read --tattattttc tgggtgagga--.

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